

GenCore version 5.1.3
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Om protein - protein search, using sw model

Run on: March 14, 2003, 05:30:50 ; Search time 1.75281 Seconds
(Without alignments) 1057.973 Million Cell updates/sec

Title: US-09-698-781-17
Perfect score: 44
Sequence: 1 TLFPVLLFL 9

Scoring table: BLOSUM52
Gapop 10.0 , Gapext 0.5

Searched: 671580 .seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %
Listing first 45 summaries

Database : SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	203	4 Q9H108	PRELIMINARY; PRT; 203 AA.
2	39	88.6	421	2 Q9FOX9	AC
3	37	84.1	604	8 Q8WG93	DT 01-MAR-2001 (TREMBLel. 16, Created)
4	35	81.8	85	Q85399	DT 01-MAR-2001 (TREMBLel. 16, Last sequence update)
5	36	81.8	161	16 Q9KNN5	DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)
6	36	81.8	227	8 Q9TBK7	DE DJ417120.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28)) (Fragment).
7	35	81.8	408	3 Q94639	DE DJ417120.1.
8	35	79.5	222	16 Q9X0H3	OS Homo sapiens (Human).
9	35	79.5	227	8 Q9B6Y8	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
10	35	79.5	316	17 Q8TRD3	OX NCBI_TAXID=9606; [1]
11	35	79.5	361	16 Q9WYL9	RP SEQUENCE FROM N.A.
12	35	79.5	501	16 Q98EG2	RA Phillipre B.;
13	35	79.5	543	16 Q99vt7	RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
14	35	79.5	543	16 Q932E9	DR EMBL; AL121974; CACI9654.1; -.
15	35	79.5	622	13 Q57661	DR HSSP; P04284; ICF.
16	35	79.5	826	2 Q8RPN1	DR Interpro; IPR001283; Allrgn_V5/Tpx1.

ALIGNMENTS

Query Match	Length	DB ID	Description
Q9H108	203	4 Q9H108	PRELIMINARY; PRT; 203 AA.
Q9H108	203	4 Q9H108	AC
Q9H108	203	4 Q9H108	DT 01-MAR-2001 (TREMBLel. 16, Created)
Q9H108	203	4 Q9H108	DT 01-MAR-2001 (TREMBLel. 16, Last sequence update)
Q9H108	203	4 Q9H108	DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)
Q9H108	203	4 Q9H108	DE DJ417120.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28)) (Fragment).
Q9H108	203	4 Q9H108	DE DJ417120.1.
Q9H108	203	4 Q9H108	OS Homo sapiens (Human).
Q9H108	203	4 Q9H108	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Q9H108	203	4 Q9H108	OX NCBI_TAXID=9606; [1]
Q9H108	203	4 Q9H108	RP SEQUENCE FROM N.A.
Q9H108	203	4 Q9H108	RA Phillipre B.;
Q9H108	203	4 Q9H108	RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
Q9H108	203	4 Q9H108	DR EMBL; AL121974; CACI9654.1; -.
Q9H108	203	4 Q9H108	DR HSSP; P04284; ICF.
Q9H108	203	4 Q9H108	DR Interpro; IPR001283; Allrgn_V5/Tpx1.
Q9H108	203	4 Q9H108	DR Pfam; PF00188; SCP; 1.
Q9H108	203	4 Q9H108	DR PRINTS; PR00837; V5PXPXLIKE.
Q9H108	203	4 Q9H108	DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
Q9H108	203	4 Q9H108	DR SMART; SM00198; SCP; 1.
Q9H108	203	4 Q9H108	DR PROSITE; PS01009; SCP_AGS_PRL_SC7_1; 1.
Q9H108	203	4 Q9H108	DR PROSITE; PS01010; SCP_AGS_PRL_SC7_2; 1.
Q9H108	203	4 Q9H108	FT NON_TER; 203
Q9H108	203	4 Q9H108	SQ SEQUENCE 203 AA; 22912 MW; F800707EE0D81a2B CRC64;

Query Match 100.0%; Score 44; DB 4; Length 203; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 TLFPVLLFL 9 Db 2 TLFPVLLFL 10

RESULT 2							
Q9FOX9	PRELIMINARY;	PRT;	421 AA.				
ID Q9FOX9							
AC 09FOX9							
DT 01-MAR-2001 (TREMBrel. 16, Created)							
DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)							
DE Putative nitrate/nitrite transporter.							
GN NARD.							
OS Pseudomonas fluorescens.							
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;							
OC Pseudomonas.							
OC NCBI_TaxID=294;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=CTRI2;							
RX MEDLINE=21240335; PubMed=11342223;							
RA Philippot L., Mirleau P., Mazurier S., Siblot S., Hartmann A.,							
RT Lemanceau P., Germon J.C.,							
RT "Characterization and transcriptional analysis of Pseudomonas							
RT fluorescens denitrifying clusters containing the nar, nir, nor and nos							
RT genes."							
RL Biochim. Biophys. Acta 1517:436-440(2001).							
DR EMBL; AF019746; AAC34311.1; -.							
SQ SEQUENCE 421 AA; 46035 MW; 49848287EBA1861 CRC64;							
Query Match Similarity 88.6%; Score 39; DB 2; Length 421;							
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;							
Qy 1 TLFVVLFL 9							
Db 314 TLFVVLFLV 322							
RESULT 3							
Q8W9G3 PRELIMINARY; PRT; 604 AA.							
ID Q8W9G3;							
AC 08W9G3;							
DT 01-MAR-2002 (TREMBrel. 20, Created)							
DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)							
DE NADH dehydrogenase subunit 5.							
GN NADH5.							
OS Tachyglossus aculeatus (Australian echidna).							
OG Mitochondrion.							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;							
OC Mammalia; Monotremata; Tachyglossidae; Tachyglossus.							
NCBI_TaxID=9261; [1]							
RP SEQUENCE FROM N.A.							
RC TISSUE=LIVER;							
RX MEDLINE=21502585; PubMed=11734900;							
RA Janke A., Meguell O., Wieczorek G., Westerman M., Arnason U.,							
RT "Phylogenetic analysis of 18S rRNA and the mitochondrial genomes of							
the wombat, <i>Vombatus ursinus</i> , and the spiny anteater, <i>Tachyglossus</i> aculeatus: Increased support for the Marsupionta Hypothesis."							
RT J. Mol. Evol. 54:71-80(2002).							
DR EMBL; AJ303116; CAC88020.1; -.							
DR InterPro; IPR003915; NADhub-oxred5.							
DR InterPro; IPR001750; Oxidored_q1.							
DR InterPro; IPR001516; Oxidored_q1_N.							
DR Pfam; PF00361; oxidored_q1_1.							
DR Pfam; PF00662; oxidored_q1_N_1.							
DR PRINTS; PR01434; NADHDHGNASE5.							
KW Mitochondrion.							
SQ SEQUENCE 604 AA; 67629 MW; 9624D7B3A3F54486 CRC64;							
Query Match Similarity 84.1%; Score 37; DB 8; Length 604;							
Best Local Similarity 77.8%; Pred. No. 65; Mismatches 0; Indels 0; Gaps 0;							
Qy 1 TLFVVLFL 9							
Db 48 SLFPVLFL 56							
RESULT 4							
Q8W9G3 PRELIMINARY; PRT; 85 AA.							
ID Q8W9G3							
AC 08W9G3;							
DT 01-Nov-1998 (TREMBrel. 08, Created)							
DT 01-Nov-1998 (TREMBrel. 08, Last sequence update)							
DE Hypothetical 10.1 kDa protein.							
OS Coxiella burnetii.							
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;							
OC Coxiella group; Coxiella.							
NCBI_TaxID=777; [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=NINE MLE PHASE I; MEDLINE=9834842; PubMed=9683477;							
RX Willemse H., Jaeger C., Baljer G.,							
RT "Physical and genetic map of the obligate intracellular bacterium							
RT Coxiella burnetii"; J. Bacteriol. 180:3816-3822(1998).							
DR EMBL; AF064956; AAC09940.1; -.							
KW Hypothetical protein.							
SQ SEQUENCE 85 AA; 10145 MW; 8F67FC9780CD1E2A CRC64;							
Query Match Similarity 81.8%; Score 36; DB 2; Length 85;							
Best Local Similarity 77.8%; Pred. No. 20; Mismatches 1; Indels 0; Gaps 0;							
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;							
Qy 1 TLFVVLFL 9							
Db 25 TAFPLLFL 33							
RESULT 5							
Q9KNN5 PRELIMINARY; PRT; 161 AA.							
ID Q9KNN5							
AC Q9KNN5;							
DT 01-OCT-2000 (TREMBrel. 15, Created)							
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)							
DE 01-DEC-2001 (TREMBrel. 19, Last annotation update)							
DE FXa protein.							
GN VC2695.							
OS Vibrio cholerae.							
OC Bacteria; Proteobacteria; gamma subdivision; vibriionaceae; vibrio.							
NCBI_TaxID=666; [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=EL TOR N16561 / SEROTYPE 01;							
RX MEDLINE=20400833; PubMed=10525301;							
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,							
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,							
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,							
RA Ermolaeva M.D., Yamaoka J., Bass S., Qin H., Dragoi I., Sellers P.,							
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,							
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,							
RA Fraser C.M.,							
RT "DNA sequence of both chromosomes of the cholera pathogen vibrio cholerae."							
RT Nature 406:477-483(2000);							
DR EMBL; AB04433; AAF95837.1; -.							
DR TIGR; VC2695; -.							
KW Complete proteome.							
SQ SEQUENCE 161 AA; 17485 MW; 04BD915C81FBEB22 CRC64;							
Query Match Similarity 81.8%; Score 36; DB 16; Length 161;							
Best Local Similarity 75.0%; Pred. No. 33; Mismatches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;							
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;							
Qy 2 LFVVLFL 9							

Db : |||:|||||
 Db 1 MPILLFL 8

RESULT 6

ID Q9PBK7 PRELIMINARY; PRT; 227 AA.

AC Q9PBK7; 1.

DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DR Pfam: PF0235; ZIP; 1.

DR TIGRFAMS; TIGR00820; zip; 1.

KW Hypothetical protein; Transmembrane; Transport.

FT TRANSMEM 64 84 POTENTIAL.

FT TRANSMEM 141 161 POTENTIAL.

FT TRANSMEM 279 299 POTENTIAL.

FT TRANSMEM 315 335 POTENTIAL.

FT TRANSMEM 408 AA; 45272 MW; 08BC0AF53CC3F0CE CRC64;

SQ SEQUENCE

Query Match 81.8%; Score 36; DB 3; Length 408;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 6; Conservative 2; MisMatches 0; Indels 0; Gaps 0;

QY 1 TLFPVLF 8
 ||||:|||

Db 281 TLFPVLF 288

RT "Phylogenetic relationships of the enigmatic hostzin (Opisthotocomus hoazin) resolved using mitochondrial and nuclear gene sequences.";
 RT Mol. Biol. Evol. 16:1300-1307(1999).

CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
 CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
 CC (BY SIMILARITY).

CC -!- SUBUNIT: F-TYPE ATPSES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.

DR EMBL; AP0168018; AAD56446.1; -.

DR HSSP; 1C17.

DR InterPro; IPR000568; ATPsynth_Asub.

DR Pfam: PF00119; ATP_synt_A; 1.

DR PRINTS: PRO0123; ATPSYNT.

DR TIGRFAMS; TIGR0131; ATP_synt_6_or_A; 1.

DR PROSITE; PS00049; ATPASE_A; 1.

KW PROSITE; PS00049; ATPASE_A; 1.

SQ SEQUENCE 227 AA; 25096 MW; 49472AE8892F0195 CRC64;

Query Match 81.8%; Score 36; DB 8; Length 227;
 Best Local Similarity 87.5%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLFPVLF 8
 ||||:|||
 Db 24 TLFPVLF 31

RESULT 7

ID 094639 PRELIMINARY; PRT; 408 AA.

AC 094639; 1.

DT 01-MAY-1999 (TREMBrel. 10, Created)
 DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DR Putative transporter C16010_06.

GN SPBC16D10_06.

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.

OC NCBI_TAXID=4896;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=972;

RA Wood V., Rajandream M.A., Barrell B.G., Brown D., Churcher C.M.,
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -!- SIMILARITY: TO YEAST ZRT1.

RESULT 8

ID Q9XH3 PRELIMINARY; PRT; 222 AA.

AC Q9XH3; 1.

DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DR Hypothetical protein TM1087.

GN TM1087.

OS Thermotoga maritima.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

OC NCBI_TAXID=2316;

OX

RN [1] SEQUENCE FROM N.A.

RP STRAIN=MGBB / DSM 3109;

RC MEDLINE=9928716; PubMed=10360571.

RX

RA Nelson K. E., Clayton R. A., Gilli S. R., Gwinn M. L., Dodson R. J.,
 RA Haft D. H., Hickey E. K., Peterson J. D., Nelson W. C., Ketchum K. A.,
 RA McDonald L., Utterback T. R., Malke J. A., Linher K. D., Garrett M. M.,
 RA Stevert A. M., Cotton M. D., Pratt M. S., Phillips C. A., Richardson D.,
 RA Heidelberg J., Sutton G. G., Fleischmann R. D., Elsen J. A., White O.,
 RA Salzberg S. L., Smith H. O., Venter J. C., Fraser C. M.,
 RA RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima";
 RA Nature 399:323-329(1999);
 RA EMBL; AED01768; AAD36164.1; -.

DR TIGR; TM1087;

DR InterPro; IPR002610; Rhomboid.

DR Pfam; PF01694; Rhomboid; 1.

KW Hypothetical protein; Complete Proteome

SQ SEQUENCE 222 AA; 25929 MW; 72793AEC17C6B50 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 222;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLFPVLF 9
 ||||:|||

Db 156 TLFPVLF 164

RESULT 9

ID 09B618 PRELIMINARY; PRT; 227 AA.

AC 09B618;

DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)

DR 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE ATP Synthase A chain (EC 3.6.1.34).

OS Casuarius bennetti (Dwarf cassowary), and
 OS Casuarius casuarius (Australian cassowary) (double-wattled cassowary).

CC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Archosauria; Aves; Palaeognathae; Casuariiformes; Casuariidae;
 OC Casuarius;
 RN NCBI_TAXID=30463; 8787;
 RP [1]
 SEQUENCE FROM N.A.
 SPECIES=C.bennetti; TISSUE=MUSCLE;
 RX MEDLINE=21055666; Published=1-217857;
 RA Cooper A., Laluzza-Fox C., Anderson S., Rambaut A., Austin J.,
 RA Ward R.;
 RT "Complete mitochondrial genome sequences of two extinct moas clarify
 ratite evolution";
 RL Nature 409:704-707(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.casuarinus;
 RX MEDLINE=21263106; Published=11370967;
 RA Haddrath O., Baker A.J.;
 RT "Complete mitochondrial DNA genome sequences of extinct birds: ratite
 phylogenetics and the vicariance biogeography hypothesis";
 RT Proc. R. Soc. Lond. B. Biol. Sci. 268:939-945(2001).
 CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
 DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE
 (BY SIMILARITY).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CORE AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
 DR EMBL: AF338713; AAK53319.1; -;
 DR InterPro: IPR000568; AIPSYNT_Asub.
 PR: PRO0019; ATPF-synt_A; 1.
 DR PRINTS: PRO00123; ATPaseA.
 DR TIGR01131; ATP_P-Sint_6_or_A; 1.
 DR PROSITE: PS00449; ATPase_A; 1.
 KW SEQUENCE 227 AA; 24981 MW; 9ASADD8ED08BFBC3 CRC64;
 SQ Query Match 79.5%; Score 35; DB 8; Length 316;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVLLF 8
 DR 111111
 DR 25 LFPVLLF 31
 RESULT 10

08TRD3 PRELIMINARY; PRT; 316 AA.
 ID 08TRD3
 AC 08TRD3; 21 (Created)
 DT 01-JUN-2002 (TREMBrel; 21, Last sequence update)
 DE Oligopeptide ABC transporter, permease.
 GN GN
 OS Methanomicrobium acetylivorans.
 OC Methanomicrobium acetylivorans.
 OC Methanomicrobium acetylivorans; Methanococci; Methanomicrobiales;
 OC Methanomicrobium acetylivorans; Methanomicrobium.
 RN NCBI_TAXID=2214;
 RP [1]
 SEQUENCE FROM N.A.
 RC STRAIN=CC-2 / ATCC 35395 / DSM 2834;
 RX MEDLINE=21939760; Published=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Attoor D., Brown A.,
 RA Allen N., Naylor J., Strange-Thomann D., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Palamas J., Turrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cain T., Graham D.B., Grahame D.A., Guss A.M.,
 RA Hederich C., Ingram-Smith C., Kuettner J.A., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RN [1]

RESULT 11

09WNL9 PRELIMINARY; PRT; 361 AA.
 ID 09WNL9
 AC 09WNL9;
 DT 01-NOV-1999 (TREMBrel; 12, Created)
 DT 01-NOV-1999 (TREMBrel; 12, Last sequence update)
 DT 01-MAR-2002 (TREMBrel; 20, Last annotation update)
 DE Hypothetical protein TM0388.
 GN TM0388.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 RN NCBI_TAXID=2336;
 RP [1]
 SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; Published=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cottontree M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima.;
 RL Nature 399:323-329(1999).
 DR EMBL: AB001718; AAD35473.1; -;
 DR TIGR; TM0388;
 DR Hypothetical Protein; Complete proteome.
 KW SEQUENCE 361 AA; 41105 MW; 729678EC49B323DA CRC64;

RESULT 12

09BBG2 PRELIMINARY; PRT; 501 AA.
 ID 09BBG2
 AC 09BBG2;
 DT 01-OCT-2001 (TREMBrel; 18, Created)
 DT 01-OCT-2001 (TREMBrel; 18, Last sequence update)
 DT 01-MAR-2002 (TREMBrel; 20, Last annotation update)
 DE Hypothetical protein M14258.
 GN M14258.
 OS Rhizobium loti (Rhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TAXID=381;
 RN [1]

RP	SEQUENCE FROM N.A.	0932E9	SEQUENCE FROM N.A.	0932E9
RC		ID	PRELIMINARY;	PRT;
RX		AC	PRT;	543 AA..
RA	MEDLINE="21082930"; PubMed=11214968;	DT	01-DEC-2001 (TREMBREL, 19, Created)	
RA	Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,	DT	01-DEC-2001 (TREMBREL, 19, Last sequence update)	
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,	DT	01-JUN-2002 (TREMBREL, 21, Last annotation update)	
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,	DE	Hypothetical protein SAV0684.	
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,	GN		
RA	Takeuchi C., Yamada M., Tabata S.;	OS	Staphylococcus aureus (strain Mu50 / ATCC 700699).	
RT	*Complete genome structure of the nitrogen-fixing symbiotic bacterium	OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;	
RT	Mesorhizobium loti.	OX	Staphylococcus.	
RL	DNA Res. 7-331-338 (2000).	RN	NCBI_TaxID=158878;	
DR	EMBL; AP003003; BAB50597.1; -.	SO	[1]	
RW	Hypothetical Protein; Complete proteome.	SEQUENCE	501 AA; 5434 MW; E70D4239DC3A929 CRC64;	
DI	28 SLEPCLLFL 36	RP	SEQUENCE FROM N.A.	
RESULT	13	RX	MEDLINE="21311952"; PubMed=11418146;	
ID	099VT7	ID	Kuroda M., Onita T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,	
AC	099VT7;	PRT;	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,	
DT	01-JUN-2001 (TREMBREL, 17, Created)	DR	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,	
DT	01-JUN-2001 (TREMBREL, 17, Last sequence update)	DR	Miutani-U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,	
DE	Hypothetical protein SA0639.	DR	Selimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,	
GN	SA0639.	RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,	
OS	Staphylococcus aureus (strain N315).	RA	Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.,	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;	RT	"Whole genome sequencing of methicillin-resistant Staphylococcus	
OC	Staphylococcus.	RT	aureus".	
OK	NEBI_TAXID=158879;	RL	Lancet 357:1225-1240(2001).	
RN	[1]	DR	EMBL; AP003300; BAB56861.1; -.	
RP	SEQUENCE FROM N.A.	DR	DR	
RK	MEDLINE=21311952; PubMed=11418146;	DR	InterPro; IPR001140; ABC_tranprtrM.	
RA	Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,	DR	DR	
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,	DR	InterPro; IPR003439; ABC_tranprtr.	
RA	Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-U.Y.,	DR	DR	
RA	Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Selimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,	DR	PFam; PR00005; ABC_membrane; 1.	
RA	Hirakawa H., Kubara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,	DR	PR00664; ABC_transportr; 1.	
RA	Ogasawara N., Hayashi H., Hiramatsu K.;	DR	PR00006; ABC_transportr; 1.	
RT	*Whole genome sequencing of methicillin-resistant Staphylococcus	DR	PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.	
RT	aureus.	DR	KW	
RT	;	DR	Hypothetical protein; Complete proteome.	
RT	Lancet 357:1225-1240(2001);	DR	SEQUENCE 543 AA; 61909 MW; 7548CBR3456AB25 CRC64;	
RA	EMBL; AP003131; BAB41872.1; -.	DR	QY	
DR	HSSE; P13569; INBD;	DR	Query Match	
DR	InterPro; IPR003593; AAA_ATPase.	DR	Best local Similarity	
DR	InterPro; IPR001140; ABCttranprtrM.	DR	79.5%;	
DR	InterPro; IPR003439; ABC_ttransportr.	DR	Pred. No.	
PFam	PF00664; ABC_membrane; 1.	DR	1.4e+02;	
PFam	PF00005; ABC_tran; 1.	DR	Mismatches	
DR	PD00006; ABC_transportr; 1.	DR	6;	
DR	SMART; SM0302; AAA; 1.	DR	Conservative	
DR	PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.	DR	2;	
KW	Hypothetical protein; Complete proteome.	DR	Mismatches	
SO	SEQUENCE 543 AA; 61909 MW; F74F7863EF364B21 CRC64;	DR	0;	
Query Match	79.5%; Score 35; DB 16; Length 543;	DR	Indels	
Best Local Similarity	75.0%; Pred. No. 1.4e+02;	DR	0;	
Matches	6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	DR	Gaps	
OY	2 LFPVLF 9	DR	0;	
DB	13 LFPVLF 20	DR	0;	
RESULT	15	DR	057661	
ID	057661;	PRT;	PRELIMINARY;	PRT;
AC	057661;	AC	622 AA.	
DT	01-JUN-1998 (TREMBREL, 06, Created)	DT		
DT	01-JUN-1998 (TREMBREL, 06, Last sequence update)	DT		
DE	01-JUN-2002 (TREMBREL, 21, Last annotation update)	DE		
DE	Intestinal sodium/lithium-dependent dicarboxylate transporter (Na ⁺)/dicarboxylate cotransporter.	DE		
DE	NADC-2.	GN		
OS	Xenopus laevis (African clawed frog).	OS		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodidae; Xenopus.	OC		
OC	Xenopus.	OC		
RN	[1]	RN		
RP	SEQUENCE FROM N.A.	RP		
RT	TISSUE-INTESTINE;	RT		
RT	MEDLINE="7423461; PubMed=9277403;	RT		
Bai L., Pajor A.M.,	RT			
RT	*Expression cloning of NADC-2, an intestinal Na ⁺ - or Li ⁺ -dependent	RT		
RT	dicarboxylate transporter.;	RT		
RT	Am. J. Physiol. 273:G267-G274(1997).	RT		
CC	-1 FUNCTION: TRANSPORTS DI- AND TRICARBOXYLATES, INCLUDING SUCCINATE, CITRATE, AND GLUTARATE, BUT EXCLUDES THE MONOCARBOXYLATE LACTATE.	CC		
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).	CC		
CC	-1 TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTESTINE.	CC		
DR	EMBL; U87318; AAB97879.1; -.	DR		
DR	InterPro; IPR001898; Na/sulf_sym.	DR		
RESULT	14	DR		

DR Pfam; PR00939; Na_sulph_sym; 1.
 DR PROSITE; PS01271; Na_Sulfate; FALSE_NaG.
 KW Transport; Transmembrane; Sodium transport; Symport.
 FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 114 134 POTENTIAL.
 FT TRANSMEM 259 279 POTENTIAL.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 366 386 POTENTIAL.
 FT TRANSMEM 411 431 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 494 514 POTENTIAL.
 FT TRANSMEM 542 562 POTENTIAL.
 FT TRANSMEM 584 604 POTENTIAL.
 FT DOMAIN 123 126 POLY-LEU.
 FT CARBOHYD 617 617 N-LINKED (GLCNAC, .) (POTENTIAL).
 SQ SEQUENCE 622 AA; 68550 MW; D25C08BB806B0098 CRC64;
 Query Match 79.5%; Score 35; DB 13; Length 622;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;
 Qy 2 LFPVLLF 8
 Db 61 LFPVLLF 67

Search completed: March 14, 2003, 05:43:02
 Job time : 4.75281 secs